

RAW SEQUENCE LISTING

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Application Serial Number: 10/536,677
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DATE: 08/15/2006

PATENT APPLICATION: US/10/536,677

TIME: 12:19:34

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4 <110> APPLICANT: Clark, Georgina Jane
5     Hart, Derek Nigel Jo
7 <120> TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS
10 <130> FILE REFERENCE: DAVI257.001APC
12 <140> CURRENT APPLICATION NUMBER: US 10/536,677
13 <141> CURRENT FILING DATE: 2005-05-27
15 <150> PRIOR APPLICATION NUMBER: PCT/AU2003/001586
16 <151> PRIOR FILING DATE: 2003-11-28
18 <150> PRIOR APPLICATION NUMBER: AU 2002952993
19 <151> PRIOR FILING DATE: 2002-11-29
22 <160> NUMBER OF SEQ ID NOS: 28
25 <170> SOFTWARE: PatentIn version 3.1
28 <210> SEQ ID NO: 1
30 <211> LENGTH: 1151
32 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
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42 acaaggaagc agagagcaga agaaaagcag aagcgaagct cagatctgct gggaggaaga      180
44 ttacattttg tccccctctg gggctcttga cagtggcagg tgacattcgt gttacaggaa      240
46 tgactgccag ggcctgggcc tcgtggcggt cttcagctct gctcctcctg cttgtcccag      300
48 gctattttcc tctgagccac cccatgaccg tggcgggccc cgtgggggga tccctgagtg      360
50 tgcagtgtcg ctatgagaag gaacacagga ccctcaacaa attctggtgc agaccaccac      420
52 agattctccg atgtgacaag attgtggaga ccaaagggtc agcagggaag aggaatggcc      480
54 gagtgtccat cagggaagc cctgcaaacc tcagcttcac agtgaccctg gagaatctca      540
56 cagaggagga cgcaggcacc tactggtgtg ggggtggatac accgtggctc cgagactttc      600
58 atgatcccat tgtcgaggtt gaggtgtccg tggtcccggc cgggacgacc acagcctcca      660
60 gccccagag ctccatgggc acctcaggtc ctcccacgaa gctgcccgtg cacacctggc      720
62 ccagcgtgac cagaaaggac agccccgaac ccagcccaca ccctggctcc ctgttcagca      780
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68 gtgagaacca gtagcatctg ctgtccatca aggcctgtg ctgcaacaga gccctctggt      960
70 ggactggaat gacctcctga ccatcaaggc ctgcaacaga gccctctggt gggactggaa     1020
72 tgacctcctg accactccct cccgggctgc tctctccaac atctcctgga atcctttgtg     1080
74 agcctccttc agccttttcc ctgtgcccga tccaacatgt gacacatgag gacttttagag     1140
76 cacaatggat c                                     1151
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83 <212> TYPE: PRT
85 <213> ORGANISM: Homo sapiens
88 <400> SEQUENCE: 2
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94 Leu Leu Val Pro Gly Tyr Phe Pro Leu Ser His Pro Met Thr Val Ala
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98 Gly Pro Val Gly Gly Ser Leu Ser Val Gln Cys Arg Tyr Glu Lys Glu
99          35          40          45
102 His Arg Thr Leu Asn Lys Phe Trp Cys Arg Pro Pro Gln Ile Leu Arg
103          50          55          60
106 Cys Asp Lys Ile Val Glu Thr Lys Gly Ser Ala Gly Lys Arg Asn Gly
107 65          70          75          80
110 Arg Val Ser Ile Arg Asp Ser Pro Ala Asn Leu Ser Phe Thr Val Thr
111          85          90          95
114 Leu Glu Asn Leu Thr Glu Glu Asp Ala Gly Thr Tyr Trp Cys Gly Val
115          100          105          110
118 Asp Thr Pro Trp Leu Arg Asp Phe His Asp Pro Ile Val Glu Val Glu
119          115          120          125
122 Val Ser Val Phe Pro Ala Gly Thr Thr Thr Ala Ser Ser Pro Gln Ser
123          130          135          140
126 Ser Met Gly Thr Ser Gly Pro Pro Thr Lys Leu Pro Val His Thr Trp
127 145          150          155          160
130 Pro Ser Val Thr Arg Lys Asp Ser Pro Glu Pro Ser Pro His Pro Gly
131          165          170          175
134 Ser Leu Phe Ser Asn Val Arg Phe Leu Leu Leu Val Leu Leu Glu Leu
135          180          185          190
138 Pro Leu Leu Leu Ser Met Leu Gly Ala Val Leu Trp Val Asn Arg Pro
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160 ggaccctcaa caaatactgg tgcagaccac cacagatttt cctatgtgac aagattgtgg 180
162 agaccaaagg gtcagcagga aaaaggaacg gccgagtgtc catcagggac agtcctgcaa 240
164 acctcagctt cacagtgacc ctggagaatc tcacagagga ggatgcaggc acctactggt 300
166 gtgggggtgga tacaccgtgg ctccgagact ttcatgatcc cgttgtcgag gttgaggtgt 360
168 ccgtgttccc ggcattcaacg tcaatgacac ctgcaagtat cactgcggcc aagacctcaa 420
170 caatcacaaac tgcattttcca cctgtatcat ccactaccct gtttgagctg ggtgccaccc 480
172 acagtgccag catccaggag gaaactgagg aggtggtgaa ctcacagctc ccgctgctcc 540
174 tctccctgct ggcattgttg ctgcttctgt tgggtggggc ctccctgcta gcctggagga 600
176 tgtttcagaa atggatcaaa gctggtgacc attcagagct gtcccagaac cccaagcagg 660
178 ctgccacgca gagtgaactg cactacgcaa atctggagct gctgatgtgg cctctgcagg 720
180 aaaagccagc accaccaagg gaggtggagg tgggaatacag cactgtggcc tccccaggg 780
182 aagaacttca ctatgcctcg gtggtgtttg attctaacac caacaggata gctgctcaga 840
184 ggcctcgggg ggaggaacca gattcagatt acagtgtgat aaggaagaca taggcttttg 900
186 tcctgcctcg ccatcggagc tctcatgggc cccaggaagt ccagggacag ctcccttata 960
188 cctggccccc gtccttctca gcctgccttc gacaacagtg accaacagac aggcagctgg 1020

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190 gtttcccagg ccacccctct gttgccatca gcttgattgg cttccccgag ggccagcagg 1080
192 gctgggggct ccggagagca gcaggaagca ctcccagcca ccagtgcctg tcgcctcttt 1140
194 cccctttgcc cctgcttcat cccagctctg tgtgtggagg acaaagcttc ttctgctg 1200
196 gctccaggaa aagatgtggc tcacgtaggt ggcacctgcc aatagctttg tcaatcacag 1260
198 ccccatagga acgtctggaa ttgcttggga gttggggaga actgtcaaga agagtgaaga 1320
200 gagtgccaaa gcggagatct gttcacctgg gggccatgga ggggggaccc actaaagatc 1380
202 aagatcaaag attctcccca tctcacagac aaggaaactg aggccagagg gaggagagaa 1440
204 ttgctcatgg ctccagaact ggtggcaagt ttctctggac tcttaggttt atttttaata 1500
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213 <212> TYPE: PRT
215 <213> ORGANISM: Homo sapiens
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225 20 25 30
228 Val Gln Cys Pro Tyr Glu Lys Glu His Arg Thr Leu Asn Lys Tyr Trp
229 35 40 45
232 Cys Arg Pro Pro Gln Ile Phe Leu Cys Asp Lys Ile Val Glu Thr Lys
233 50 55 60
236 Gly Ser Ala Gly Lys Arg Asn Gly Arg Val Ser Ile Arg Asp Ser Pro
237 65 70 75 80
240 Ala Asn Leu Ser Phe Thr Val Thr Leu Glu Asn Leu Thr Glu Glu Asp
241 85 90 95
244 Ala Gly Thr Tyr Trp Cys Gly Val Asp Thr Pro Trp Leu Arg Asp Phe
245 100 105 110
248 His Asp Pro Val Val Glu Val Glu Val Ser Val Phe Pro Ala Ser Thr
249 115 120 125
252 Ser Met Thr Pro Ala Ser Ile Thr Ala Ala Lys Thr Ser Thr Ile Thr
253 130 135 140
256 Thr Ala Phe Pro Pro Val Ser Ser Thr Thr Leu Phe Ala Val Gly Ala
257 145 150 155 160
260 Thr His Ser Ala Ser Ile Gln Glu Glu Thr Glu Glu Val Val Asn Ser
261 165 170 175
264 Gln Leu Pro Leu Leu Ser Leu Leu Ala Leu Leu Leu Leu Leu
265 180 185 190
268 Val Gly Ala Ser Leu Leu Ala Trp Arg Met Phe Gln Lys Trp Ile Lys
269 195 200 205
272 Trp Ile Lys Ala Gly Asp His Ser Glu Leu Ser Gln Asn Pro Lys Gln
273 210 215 220
276 Ala Ala Thr Gln Ser Glu Leu His Tyr Ala Asn Leu Glu Leu Leu Met
277 225 230 235 240
280 Trp Pro Leu Gln Glu Lys Pro Ala Pro Pro Arg Glu Val Glu Val Glu
281 245 250 255
284 Tyr Ser Thr Val Ala Ser Pro Arg Glu Glu Leu His Tyr Ala Ser Val
285 260 265 270
288 Val Phe Asp Ser Asn Thr Asn Arg Ile Ala Ala Gln Arg Pro Arg Glu

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310 gctctgtgac tggcactgcg ggggactctc tgacagtgtg gtgtcagtat gagagcatgt      180
312 acaagggata taacaagtac tggtgccgag gacagtacga cacgtcatgt gagagcattg      240
314 tggagaccaa gggagaagag aaggtggaga ggaatggccg cgtgtccatc agagaccacc      300
316 cggaggctct cgccttcact gtgaccatgc agaacctcaa tgaagatgat gctggatctt      360
318 actggtgcaa aattcagaca gtgtgggtcc tggattcatg gtcacgcgat ccctcggacc      420
320 tggttagggt gtatgtttcc ccagcaatta caaccccaag gaggaccaca catccagcca      480
322 cacctcccat cttcctggtg gtgaaccctg ggcgaaacct cagcaccagg gaggtgttga      540
324 cccaaaattc agggttccgg ctcagcagcc ctcacttctt gctcgtggtc cttctgaagc      600
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341 <400> SEQUENCE: 6
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348          20          25          30
351 Thr Val Trp Cys Gln Tyr Glu Ser Met Tyr Lys Gly Tyr Asn Lys Tyr
352          35          40          45
355 Trp Cys Arg Gly Gln Tyr Asp Thr Ser Cys Glu Ser Ile Val Glu Thr
356          50          55          60
359 Lys Gly Glu Glu Lys Val Glu Arg Asn Gly Arg Val Ser Ile Arg Asp
360 65          70          75          80
363 His Pro Glu Ala Leu Ala Phe Thr Val Thr Met Gln Asn Leu Asn Glu
364          85          90          95
367 Asp Asp Ala Gly Ser Tyr Trp Cys Lys Ile Gln Thr Val Trp Val Leu
368          100         105         110
371 Asp Ser Trp Ser Arg Asp Pro Ser Asp Leu Val Arg Val Tyr Val Ser
372          115         120         125
375 Pro Ala Ile Thr Thr Pro Arg Arg Thr Thr His Pro Ala Thr Pro Pro
376          130         135         140
379 Ile Phe Leu Val Val Asn Pro Gly Arg Asn Leu Ser Thr Arg Glu Val
380 145         150         155         160
383 Leu Thr Gln Asn Ser Gly Phe Arg Leu Ser Ser Pro His Phe Leu Leu
384          165         170         175
387 Val Val Leu Leu Lys Leu Pro Leu Leu Leu Ser Met Leu Gly Ala Val
388          180         185         190

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409 tatggctcag gctgggagac ctacttgaag tggcggtgtc aaggagctga ttggaattac      180
411 tgtaacatcc ttgttaaaac aaatggatca gagcaggagg taaagaagaa tcgagtttcc      240
413 atcagggaca atcagaaaaa ccacgtgttc accgtgacca tggagaatct caaaagagat      300
415 gatgctgaca gttattggtg tgggactgag agacctggaa ttgatcttgg ggtcaaagtt      360
417 caagtgacca ttaaccacgc tcagtgcctg agtctgttgc ccacagatga cagggtgatg      420
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440      20      25      30
443 Gly Ser Glu Gln Gly Ser Leu Thr Val Gln Cys Ala Tyr Gly Ser Gly
444      35      40      45
447 Trp Glu Thr Tyr Leu Lys Trp Arg Cys Gln Gly Ala Asp Trp Asn Tyr
448      50      55      60
451 Cys Asn Ile Leu Val Lys Thr Asn Gly Ser Glu Gln Glu Val Lys Lys
452 65      70      75      80
455 Asn Arg Val Ser Ile Arg Asp Asn Gln Lys Asn His Val Phe Thr Val
456      85      90      95
459 Thr Met Glu Asn Leu Lys Arg Asp Asp Ala Asp Ser Tyr Trp Cys Gly
460      100      105      110
463 Thr Glu Arg Pro Gly Ile Asp Leu Gly Val Lys Val Gln Val Thr Ile
464      115      120      125
467 Asn Pro Ala Gln Cys Leu Ser Leu Leu Pro Thr Asp Asp Arg Val Met
468      130      135      140
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472 145      150      155      160
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VERIFICATION SUMMARY

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